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Sequence Listing was accepted.

See attached Validation Report.

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217-9197 (toll free).

Reviewer: markspencer

Timestamp: [year=2008; month=9; day=15; hr=9; min=15; sec=11; ms=141; ]

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Application No: 10797262 Version No: 3.0

Input Set:

Output Set:

Started: 2008-09-14 21:20:19.717  
Finished: 2008-09-14 21:20:25.314  
Elapsed: 0 hr(s) 0 min(s) 5 sec(s) 597 ms  
Total Warnings: 16  
Total Errors: 1  
No. of SeqIDs Defined: 18  
Actual SeqID Count: 18

Error code	Error Description
W 402	Undefined organism found in <213> in SEQ ID (1)
W 402	Undefined organism found in <213> in SEQ ID (2)
W 402	Undefined organism found in <213> in SEQ ID (3)
W 213	Artificial or Unknown found in <213> in SEQ ID (4)
W 213	Artificial or Unknown found in <213> in SEQ ID (5)
W 213	Artificial or Unknown found in <213> in SEQ ID (6)
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W 213	Artificial or Unknown found in <213> in SEQ ID (9)
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W 213	Artificial or Unknown found in <213> in SEQ ID (17)
W 213	Artificial or Unknown found in <213> in SEQ ID (18)

## SEQUENCE LISTING

<110> East Tennessee State University Research Foundation  
Lampson, Bert  
Veloire, Jashree

<120> RNA-DEPENDENT DNA POLYMERASE FROM GEOBACILLUS STEAROTHERMOPHILUS

<130> 2826067.000002

<140> 10797262

<141> 2004-03-10

<160> 18

<170> PatentIn version 3.5

<210> 1

<211> 1263

<212> DNA

<213> Geobacillus stearothermophilus

<220>

<221> CDS

<222> (1)..(1263)

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1                  5                  10                  15	

ctc aaa cgg gtc gaa gcc aac caa gga gca ccg gga atc gac gga gta	96
Leu Lys Arg Val Glu Ala Asn Gln Gly Ala Pro Gly Ile Asp Gly Val	
20                  25                  30	

tca acc gat caa ctc cgt gat tac atc cgc gct cac tgg agc acg atc	144
Ser Thr Asp Gln Leu Arg Asp Tyr Ile Arg Ala His Trp Ser Thr Ile	
35                  40                  45	

cgc gcc caa ctc ttg gcg gga acc tac cgg ccg gcg cct gtc cgc agg	192
Arg Ala Gln Leu Leu Ala Gly Thr Tyr Arg Pro Ala Pro Val Arg Arg	
50                  55                  60	

gtc gga atc ccg aaa ccg ggc ggc ggc aca cgg cag cta ggc att ccc	240
Val Gly Ile Pro Lys Pro Gly Gly Gly Thr Arg Gln Leu Gly Ile Pro	
65                  70                  75                  80	

acc gtg gtg gac cgg ctg atc caa caa gcc att ctt caa gaa ctc aca	288
Thr Val Val Asp Arg Leu Ile Gln Gln Ala Ile Leu Gln Glu Leu Thr	
85                  90                  95	

ccc att ttc gat cca gac ttc tcc cct tcc agc ttc gga ttc cgt ccg	336
Pro Ile Phe Asp Pro Asp Phe Ser Pro Ser Ser Phe Gly Phe Arg Pro	
100                  105                  110	

ggc cgt aac gcc cac gat gcc gtg cgg caa gcg caa ggc tac atc cag	384
Gly Arg Asn Ala His Asp Ala Val Arg Gln Ala Gln Gly Tyr Ile Gln	
115 120 125	
gaa ggg tat cgg tac gtg gtc gac atg gac ctg gaa aag ttc ttt gat	432
Glu Gly Tyr Arg Tyr Val Val Asp Met Asp Leu Glu Lys Phe Phe Asp	
130 135 140	
cgg gtc aac cat gac atc ttg atg agt cgg gtg gcc cga aaa gtc aag	480
Arg Val Asn His Asp Ile Leu Met Ser Arg Val Ala Arg Lys Val Lys	
145 150 155 160	
gat aaa cgc gtg ctg aaa ctg atc cgt gcc tac ctg caa gcc ggc gtt	528
Asp Lys Arg Val Leu Lys Leu Ile Arg Ala Tyr Leu Gln Ala Gly Val	
165 170 175	
atg atc gaa ggg gtg aag gtg cag acg gag gaa ggg acg ccg caa ggc	576
Met Ile Glu Gly Val Lys Val Gln Thr Glu Glu Gly Thr Pro Gln Gly	
180 185 190	
ggc ccc ctc agc ccc ctg ctg gcg aac atc ctt ctc gac gat tta gac	624
Gly Pro Leu Ser Pro Leu Leu Ala Asn Ile Leu Leu Asp Asp Leu Asp	
195 200 205	
aag gaa ttg gag aag cga gga ttg aaa ttc tgc cgt tac gca gat gac	672
Lys Glu Leu Glu Lys Arg Gly Leu Lys Phe Cys Arg Tyr Ala Asp Asp	
210 215 220	
tgc aac atc tat gtg aaa agt ctg cgg gca gga caa cgg gtg aaa caa	720
Cys Asn Ile Tyr Val Lys Ser Leu Arg Ala Gly Gln Arg Val Lys Gln	
225 230 235 240	
agc atc caa cgg ttc ttg gag aaa acg ctc aaa ctc aaa gta aac gag	768
Ser Ile Gln Arg Phe Leu Glu Lys Thr Leu Lys Leu Lys Val Asn Glu	
245 250 255	
gag aaa agt gcg gtg gac cgc ccg tgg aaa cgg gcc ttt ctg ggg ttt	816
Glu Lys Ser Ala Val Asp Arg Pro Trp Lys Arg Ala Phe Leu Gly Phe	
260 265 270	
agc ttc aca ccg gaa cga aaa gcg cga atc cgg ctc gcc cca agg tcg	864
Ser Phe Thr Pro Glu Arg Lys Ala Arg Ile Arg Leu Ala Pro Arg Ser	
275 280 285	
att caa cgt ctg aaa cag cgg att cga cag ctg acc aac cca aac tgg	912
Ile Gln Arg Leu Lys Gln Arg Ile Arg Gln Leu Thr Asn Pro Asn Trp	
290 295 300	
agc ata tcg atg cca gaa cga att cat cgc gtc aat caa tac gtc atg	960
Ser Ile Ser Met Pro Glu Arg Ile His Arg Val Asn Gln Tyr Val Met	
305 310 315 320	
gga tgg atc ggg tat ttt cgg ctc gtc gaa acc ccg tct gtc ctt cag	1008
Gly Trp Ile Gly Tyr Phe Arg Leu Val Glu Thr Pro Ser Val Leu Gln	
325 330 335	
acc atc gaa gga tgg att cgg agg agg ctt cga ctc tgt caa tgg ctt	1056

Thr Ile Glu Gly Trp Ile Arg Arg Arg Leu Arg Leu Cys Gln Trp Leu  
 340 345 350

caa tgg aaa cgg gtc aga acc aga atc cgt gag tta aga gcg ctg ggg 1104  
 Gln Trp Lys Arg Val Arg Thr Arg Ile Arg Glu Leu Arg Ala Leu Gly  
 355 360 365

ctg aaa gag aca gcg gtg atg gag atc gcc aat acc cga aaa gga gct 1152  
 Leu Lys Glu Thr Ala Val Met Glu Ile Ala Asn Thr Arg Lys Gly Ala  
 370 375 380

tgg cga aca acg aaa acg ccg caa ctc cac cag gcc ctg ggc aaa acc 1200  
 Trp Arg Thr Thr Lys Thr Pro Gln Leu His Gln Ala Leu Gly Lys Thr  
 385 390 395 400

tac tgg acc gct caa ggg ctc aag agt ttg acg caa cga tat ttc gaa 1248  
 Tyr Trp Thr Ala Gln Gly Leu Lys Ser Leu Thr Gln Arg Tyr Phe Glu  
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ctc cgt caa ggt tga 1263  
 Leu Arg Gln Gly  
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 <212> PRT  
 <213> Geobacillus stearothermophilus

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Ser Thr Asp Gln Leu Arg Asp Tyr Ile Arg Ala His Trp Ser Thr Ile  
 35 40 45

Arg Ala Gln Leu Leu Ala Gly Thr Tyr Arg Pro Ala Pro Val Arg Arg  
 50 55 60

Val Gly Ile Pro Lys Pro Gly Gly Gly Thr Arg Gln Leu Gly Ile Pro  
 65 70 75 80

Thr Val Val Asp Arg Leu Ile Gln Gln Ala Ile Leu Gln Glu Leu Thr  
 85 90 95

Pro Ile Phe Asp Pro Asp Phe Ser Pro Ser Ser Phe Gly Phe Arg Pro  
 100 105 110

Gly Arg Asn Ala His Asp Ala Val Arg Gln Ala Gln Gly Tyr Ile Gln  
115 120 125

Glu Gly Tyr Arg Tyr Val Val Asp Met Asp Leu Glu Lys Phe Phe Asp  
130 135 140

Arg Val Asn His Asp Ile Leu Met Ser Arg Val Ala Arg Lys Val Lys  
145 150 155 160

Asp Lys Arg Val Leu Lys Leu Ile Arg Ala Tyr Leu Gln Ala Gly Val  
165 170 175

Met Ile Glu Gly Val Lys Val Gln Thr Glu Glu Gly Thr Pro Gln Gly  
180 185 190

Gly Pro Leu Ser Pro Leu Leu Ala Asn Ile Leu Leu Asp Asp Leu Asp  
195 200 205

Lys Glu Leu Glu Lys Arg Gly Leu Lys Phe Cys Arg Tyr Ala Asp Asp  
210 215 220

Cys Asn Ile Tyr Val Lys Ser Leu Arg Ala Gly Gln Arg Val Lys Gln  
225 230 235 240

Ser Ile Gln Arg Phe Leu Glu Lys Thr Leu Lys Leu Lys Val Asn Glu  
245 250 255

Glu Lys Ser Ala Val Asp Arg Pro Trp Lys Arg Ala Phe Leu Gly Phe  
260 265 270

Ser Phe Thr Pro Glu Arg Lys Ala Arg Ile Arg Leu Ala Pro Arg Ser  
275 280 285

Ile Gln Arg Leu Lys Gln Arg Ile Arg Gln Leu Thr Asn Pro Asn Trp  
290 295 300

Ser Ile Ser Met Pro Glu Arg Ile His Arg Val Asn Gln Tyr Val Met  
305 310 315 320

Gly Trp Ile Gly Tyr Phe Arg Leu Val Glu Thr Pro Ser Val Leu Gln  
325 330 335

Thr Ile Glu Gly Trp Ile Arg Arg Arg Leu Arg Leu Cys Gln Trp Leu  
340 345 350

Gln Trp Lys Arg Val Arg Thr Arg Ile Arg Glu Leu Arg Ala Leu Gly  
355 360 365

Leu Lys Glu Thr Ala Val Met Glu Ile Ala Asn Thr Arg Lys Gly Ala  
370 375 380

Trp Arg Thr Thr Lys Thr Pro Gln Leu His Gln Ala Leu Gly Lys Thr  
385 390 395 400

Tyr Trp Thr Ala Gln Gly Leu Lys Ser Leu Thr Gln Arg Tyr Phe Glu  
405 410 415

Leu Arg Gln Gly  
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<211> 420  
<212> PRT  
<213> *Geobacillus stearothermophilus*

<220>  
<221> PEPTIDE  
<222> (1)..(420)

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Ser Thr Asp Gln Leu Arg Asp Tyr Ile Arg Ala His Trp Ser Thr Ile  
35 40 45

Arg Ala Gln Leu Leu Ala Gly Thr Tyr Arg Pro Ala Pro Val Arg Arg  
50 55 60

Val Gly Ile Pro Lys Pro Gly Gly Gly Thr Arg Gln Leu Gly Ile Pro  
65 70 75 80

Thr Val Val Asp Arg Leu Ile Gln Gln Ala Ile Leu Gln Glu Leu Thr  
85 90 95

Pro Ile Phe Asp Pro Asp Phe Ser Pro Ser Ser Phe Gly Phe Arg Pro  
100 105 110

Gly Arg Asn Ala His Asp Ala Val Arg Gln Ala Gln Gly Tyr Ile Gln  
115 120 125

Glu Gly Tyr Arg Tyr Val Val Asp Met Asp Leu Glu Lys Phe Phe Asp  
130 135 140

Arg Val Asn His Asp Ile Leu Met Ser Arg Val Ala Arg Lys Val Lys  
145 150 155 160

Asp Lys Arg Val Leu Lys Leu Ile Arg Ala Tyr Leu Gln Ala Gly Val  
165 170 175

Met Ile Glu Gly Val Lys Val Gln Thr Glu Glu Gly Thr Pro Gln Gly  
180 185 190

Gly Pro Leu Ser Pro Leu Leu Ala Asn Ile Leu Leu Asp Asp Leu Asp  
195 200 205

Lys Glu Leu Glu Lys Arg Gly Leu Lys Phe Cys Arg Tyr Ala Asp Asp  
210 215 220

Cys Asn Ile Tyr Val Lys Ser Leu Arg Ala Gly Gln Arg Val Lys Gln  
225 230 235 240

Ser Ile Gln Arg Phe Leu Glu Lys Thr Leu Lys Leu Lys Val Asn Glu  
245 250 255

Glu Lys Ser Ala Val Asp Arg Pro Trp Lys Arg Ala Phe Leu Gly Phe  
260 265 270

Ser Phe Thr Pro Glu Arg Lys Ala Arg Ile Arg Leu Ala Pro Arg Ser  
275 280 285

Ile Gln Arg Leu Lys Gln Arg Ile Arg Gln Leu Thr Asn Pro Asn Trp  
290 300

Ser Ile Ser Met Pro Glu Arg Ile His Arg Val Asn Gln Tyr Val Met



305 310 315 320

Gly Trp Ile Gly Tyr Phe Arg Leu Val Glu Thr Pro Ser Val Leu Gln  
325 330 335

Thr Ile Glu Gly Trp Ile Arg Arg Arg Leu Arg Leu Cys Gln Trp Leu  
340 345 350

Gln Trp Lys Arg Val Arg Thr Arg Ile Arg Glu Leu Arg Ala Leu Gly  
355 360 365

Leu Lys Glu Thr Ala Val Met Glu Ile Ala Asn Thr Arg Lys Gly Ala  
370 375 380

Trp Arg Thr Thr Lys Thr Pro Gln Leu His Gln Ala Leu Gly Lys Thr  
385 390 395 400

Tyr Trp Thr Ala Gln Gly Leu Lys Ser Leu Thr Gln Arg Tyr Phe Glu  
405 410 415

Leu Arg Gln Gly  
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aacgcattctt agcgagagac aacctcatca cggcgctcaa acgggtcgaa gccaaccaag 180  
gagcaccggg aatcgacgga gtatcaaccg atcaactccg tgattacatc cgcgctcact 240  
ggagcacgat ccgcgccaa ctcttggcgg gaacctaccg gccggcgccct gtccgcaggg 300  
tcggaatccc gaaaccgggc ggcggcacac ggcagctagg cattcccacc gtggtggacc 360

ggctgatcca acaagccatt cttcaagaac tcacacccat tttcgatcca gacttctccc	420
cttcagctt cggattccgt cggggccgta acgcccacga tgccgtgcgg caagcgcaag	480
gctacatcca ggaagggtat cggtagctgg tcgacatgga cctggaaaag ttctttgatc	540
gggtcaacca tgacatcttg atgagtcggg tggcccgaag agtcaaggat aaacgcgtgc	600
tgaaactgat ccgtgcctac ctgcaagccg gcgttatgat cgaaggggtg aaggtgcaga	660
cggaggaagg gacgccgcaa ggccggcccc tcagccccct gctggcgaac atccttctcg	720
acgatttaga caaggaattg gagaagcgag gattgaaatt ctgccgttac gcagatgact	780
gcaacatcta tgtgaaaagt ctgcgggcag gacaacgggt gaaacaaagc atccaacggt	840
tcttgagaga aacgctcaaa ctcaaagtaa acgaggagaa aagtgcggtg gaccgcccg	900
ggaaacgggc ctttctgggg tttagcttca caccggaacg aaaagcgcg atccggctcg	960
ccccaaagtc gattcaacgt ctgaaacagc ggattcgaca gctgaccaac ccaaactgga	1020
gcatatcgat gccagaacga attcatcgcg tcaatcaata cgtcatggga tggatcgggt	1080
attttcggct cgtcgaaacc ccgtctgtcc ttcagaccat cgaaggatgg attcggagga	1140
ggcttcgact ctgtcaatgg cttcaatgga aacgggtcag aaccagaatc cgtgagttaa	1200
gagcgctggg gctgaaagag acagcgggtg tggagatcgc caatacccg aaaggagctt	1260
ggcgaacaac gaaaacgcc caactccacc aggcctggg caaacctac tggaccgctc	1320
aagggtcaa gagtttgacg caacgatatt tcgaactccg tcaaggttga	1370

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<220>  
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<222> (1)..(455)

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Arg Gly Ser His Met Arg Gln Asp Leu Asn Leu Ile Pro Arg Lys Glu  
20 25 30

Lys Ile Thr Met Ala Leu Leu Glu Arg Ile Leu Ala Arg Asp Asn Leu  
35 40 45

Ile Thr Ala Leu Lys Arg Val Glu Ala Asn Gln Gly Ala Pro Gly Ile  
50 55 60